SEQUENCE LISTING

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<120> A METHOD FOR IMPROVING THE THERMOSTABILITY OF SUCROSE PHOSPHORYLASE (SP)

<130> EG014US

<140> PCT/JP2004/012533
<141> 2004-08-31

<150> JP2003-313305
<151> 2003-09-04

<160> 27

<170> PatentIn version 3.3

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gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt      144
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
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gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt      192
Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
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ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
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gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta      336
Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
            100                 105                 110

aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg      384
Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
        115                 120                 125

gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa      432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
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ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa      480
Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
                165                 170                 175

tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg      576
Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt      624
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gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act      720
Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcc      768
Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt      816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
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gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
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gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc      960
Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc     1008
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    370                 375                 380

ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt     1200
Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt     1248
Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat     1296
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ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa     1344
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cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc     1392
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    450                 455                 460

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Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
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Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
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Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
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145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
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Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
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Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
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Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
            340                 345                 350
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Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
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Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
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Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
            420                 425                 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
        435                 440                 445

Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
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gga aat aat ctt aaa gac tta tat gat aat ttg gaa gag cat ttt gga       96
Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly
            20                  25                  30

gat gct att gga gga gtt cac ctt tta cca ttt ttc cca tca aca gtt      144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Val
        35                  40                  45

gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gac tca gct ttt      192
Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
    50                  55                  60

ggt gat tgg gag gat gtg aag cgt tta ggt gag aaa tat tat ctt atg      240
Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttt atg att aat cat att tct cgt caa tcc aag tat tat aag      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gct ctc ttt tta      336
Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu
            100                 105                 110

aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta      384
Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
        115                 120                 125

gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtg      432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
    130                 135                 140

ttt gaa gat ggt tca gtg gaa cat ttg tgg aat acc ttt ggt gag gag      480
Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
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145                 150                 155                 160

cag att gat ctt gat gtg acc aaa gaa gta act atg gaa ttt atc cgt      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
                165                 170                 175

aag acc att cag cac ttg gca agt aat ggg tgt gat ttg att cgt cta      576
Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gct tat gca gtg aag aaa ttg gat act aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gtg gaa cca gat att tgg gat tta ttg gac aaa gtt cga gat atc gct      672
Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

gct gag tat ggg aca gag ctt tta cct gag att cat gaa cac tat tcg      720
Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

att cag ttt aaa ata gca gac cat gat tac tat gtt tat gat ttt gct      768
Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

ctt cca atg gtg aca ctt tat act ctt tac agt tcc aga aca gag cgt      816
Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
            260                 265                 270

ttg gct aag tgg tta aag atg agc ccg atg aag caa ttt acg acg cta      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat acc cat gat ggg att gga gta gta gat gtc aag gat atc ctg acc      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

gat gag gag att gac tat gct tca aat gaa ctc tat aag gtt gga gcc      960
Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtc aaa cgt aag tac tct agt gcc gag tat aac aac tta gat atc     1008
Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tac caa atc aat tca acc tac tat tca gcg ctt gga gat gat gat gtc     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
            340                 345                 350

aag tat ttt ctc gct cgt cta att caa gct ttt gcc cca ggt att cct     1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

cag att tac tat gtg ggt cta tta gca ggc aag aat gac ttg aaa tta     1152
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    370                 375                 380

tta gaa gaa act aaa gaa ggt cga aat att aat cgt cat tac tat agc     1200
Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

aac gag gaa ata gca aaa gaa gtg caa cga cct gtt gtg aag gcc ctt     1248
Asn Glu Glu Ile Ala Lys Glu Val Gln Arg Pro Val Val Lys Ala Leu
                405                 410                 415

ctc aat cta ttt tct ttc cgt aac cgt tca gaa gcc ttt gat cta gaa     1296
Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Glu Ala Phe Asp Leu Glu
            420                 425                 430

ggg act act gag ata gag aca cca aca gct cac agc att gta atc aaa     1344
Gly Thr Thr Glu Ile Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
        435                 440                 445

cgt caa aat aaa gat aag tcc gta aca gca gta gta gaa att gat ttg     1392
Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Val Glu Ile Asp Leu
    450                 455                 460

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        35                  40                  45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
    50                  55                  60

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu
            100                 105                 110

Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
    130                 135                 140

Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
                165                 170                 175

Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
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Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320
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Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
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Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
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Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
    370                 375                 380

Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Asn Glu Glu Ile Ala Lys Glu Val Gln Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Glu Ala Phe Asp Leu Glu
            420                 425                 430

Gly Thr Thr Glu Ile Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
        435                 440                 445

Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Val Glu Ile Asp Leu
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ggt agg aac cta aaa gag ctg gat gaa aat atc agc atc tat ttt gga       96
Gly Arg Asn Leu Lys Glu Leu Asp Glu Asn Ile Ser Ile Tyr Phe Gly
            20                  25                  30

gat gca att gga ggc gtc cat ctc ctg cct ttc ttc ccc tcg aca gga      144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat agg gga ttc gct cca gtt gat tac gat aag gtg gat cct gct ttt      192
Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Lys Val Asp Pro Ala Phe
    50                  55                  60

ggt gac tgg gat gat gtc aaa cgt tta ggt gct aaa tac tac ctg atg      240
Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Ala Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttt atg att aat cat atc tcc cgt caa tct aag tat tat aag      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

gat ttt caa gag aaa aaa gat gct tct gac tat gcg gat tta ttt ctg      336
Asp Phe Gln Glu Lys Lys Asp Ala Ser Asp Tyr Ala Asp Leu Phe Leu
            100                 105                 110

cgc tgg gaa aaa ttc tgg ccg gaa aac cgt ccc acc caa gca gat att      384
Arg Trp Glu Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ala Asp Ile
        115                 120                 125

gat tta att tat aaa cgt aaa gac aag gct cct atg cag gag att gtc      432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Met Gln Glu Ile Val
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    130                 135                 140

ttc gcc gat gga acc aaa gaa cat ctc tgg aat act ttc gga gaa gag      480
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145                 150                 155                 160

caa att gat cta gat gtt act aaa gaa gtg acc atg gac ttt atc aaa      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Lys
                165                 170                 175

aaa aac atc gag cat cta gca gtc aat ggt tgt gat ctc att cgc ctg      576
Lys Asn Ile Glu His Leu Ala Val Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gcc tac gcc gtg aaa aaa ttg gac act aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gtc gaa cca gaa att tgg gat ctc cta acc aag gta cag aca atc gcc      672
Val Glu Pro Glu Ile Trp Asp Leu Leu Thr Lys Val Gln Thr Ile Ala
    210                 215                 220

aag gaa gca ggg gca gat atc ctg ccg gaa ata cat gag cat tat tct      720
Lys Glu Ala Gly Ala Asp Ile Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

atc cag ttc aaa att gct gag cat gac tat ttc att tat gat ttt gcc      768
Ile Gln Phe Lys Ile Ala Glu His Asp Tyr Phe Ile Tyr Asp Phe Ala
                245                 250                 255

ctt cca atg gta acc ctt tac tct ctt tat agc ggt agg gtg caa cgt      816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Arg Val Gln Arg
            260                 265                 270

ttg gca gat tgg ctg gct aaa agt cct atg aag caa ttt act acg ctg      864
Leu Ala Asp Trp Leu Ala Lys Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat acc cat gat ggc att gga gtt gta gat gtt aaa gat atc ttg aca      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

gac gag gaa att gct tac act tcc gat caa ctc tac aag gtt gga gcc      960
Asp Glu Glu Ile Ala Tyr Thr Ser Asp Gln Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aac gtc aat cgc aaa tat tca acg gca gaa tat aat aac ctt gat att     1008
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tat caa atc aac tcg acc tac tat tca gcc ctt ggt gac gat gac aag     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
            340                 345                 350

aag tat ttc tta gct cgt ctc att caa gct ttt gca cca ggg att cca     1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
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caa gtt tat tat gtt gga ctt ttg gct gga aaa aac gat ctg aag ctc     1152
Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
    370                 375                 380

ttg gaa aaa acc aag gaa ggt cgc aat atc aat cgt cat tat tat agc     1200
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385                 390                 395                 400

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                405                 410                 415

atc aaa ctg ttt agc tat cgc aac aac tct caa gct ttc gac tta gac     1296
Ile Lys Leu Phe Ser Tyr Arg Asn Asn Ser Gln Ala Phe Asp Leu Asp
            420                 425                 430

ggc agc ctt gaa acg gaa gtt ctg gat gac cac acc atc gtt atc aag     1344
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        435                 440                 445

cgt tct aat cag gac aag agt gct tta gct caa gct gtt att aat ttg     1392
Arg Ser Asn Gln Asp Lys Ser Ala Leu Ala Gln Ala Val Ile Asn Leu
    450                 455                 460

caa gat tta acc tat cag gtc act gag aat ggt caa acc att aca ttc     1440
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465                 470                 475                 480
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gaa 1443
Glu

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<213> Streptococcus sorbinus

<400> 6

Met Thr Leu Thr Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu
1 5 10 15

Gly Arg Asn Leu Lys Glu Leu Asp Glu Asn Ile Ser Ile Tyr Phe Gly
20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Lys Val Asp Pro Ala Phe
50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Ala Lys Tyr Tyr Leu Met
65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
85 90 95

Asp Phe Gln Glu Lys Lys Asp Ala Ser Asp Tyr Ala Asp Leu Phe Leu
100 105 110

Arg Trp Glu Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ala Asp Ile
115 120 125

Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Met Gln Glu Ile Val
130 135 140

Phe Ala Asp Gly Thr Lys Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145 150 155 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Lys
165 170 175

Lys Asn Ile Glu His Leu Ala Val Asn Gly Cys Asp Leu Ile Arg Leu
180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Thr Lys Val Gln Thr Ile Ala
210 215 220

Lys Glu Ala Gly Ala Asp Ile Leu Pro Glu Ile His Glu His Tyr Ser
225 230 235 240

Ile Gln Phe Lys Ile Ala Glu His Asp Tyr Phe Ile Tyr Asp Phe Ala
245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Arg Val Gln Arg
260 265 270

Leu Ala Asp Trp Leu Ala Lys Ser Pro Met Lys Gln Phe Thr Thr Leu
275 280 285

```
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Ala Tyr Thr Ser Asp Gln Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
            340                 345                 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
    370                 375                 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Ser Glu Glu Ile Ala His Glu Val Glu Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Ile Lys Leu Phe Ser Tyr Arg Asn Asn Ser Gln Ala Phe Asp Leu Asp
            420                 425                 430

Gly Ser Leu Glu Thr Glu Val Leu Asp Asp His Thr Ile Val Ile Lys
        435                 440                 445

Arg Ser Asn Gln Asp Lys Ser Ala Leu Ala Gln Ala Val Ile Asn Leu
    450                 455                 460

Gln Asp Leu Thr Tyr Gln Val Thr Glu Asn Gly Gln Thr Ile Thr Phe
465                 470                 475                 480

Glu
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<210> 7
<211> 1470
<212> DNA
<213> Leuconostoc mesenteroides

<220>
<221> CDS
<222> (1)..(1470)

<400> 7

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atg gaa att caa aac aaa gca atg ttg atc act tat gct gat tcg ttg      48
Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                  10                  15

ggc aaa aac tta aaa gat gtt cat caa gtc ttg aaa gaa gat att gga      96
Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly
            20                  25                  30

gat gcg att ggt ggg gtt cat ttg ttg cct ttc ttc cct tca aca ggt     144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat cgc ggt ttt gcg cca gcc gat tat act cgt gtt gat gcc gca ttt     192
Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe
    50                  55                  60

ggt gat tgg gca gat gtc gaa gca ttg ggt gaa gaa tac tat ttg atg     240
Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met
65                  70                  75                  80

ttt gac ttc atg att aac cat att tct cgt gaa tca gtg atg tat caa     288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln
```

```
                85                  90                  95

gat ttt aag aag aat cat gac gat tca aag tat aaa gat ttc ttt att      336
Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile
            100                 105                 110

cgt tgg gaa aag ttc tgg gca aag gcc ggc gaa aac cgt cca aca caa      384
Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln
        115                 120                 125

gcc gat gtt gac tta att tac aag cgt aaa gat aag gca cca acg caa      432
Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln
    130                 135                 140

gaa atc act ttt gat gat ggc aca aca gaa aac ttg tgg aat act ttt      480
Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe
145                 150                 155                 160

ggt gaa gaa caa att gac att gat gtt aat tca gcc att gcc aag gaa      528
Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu
                165                 170                 175

ttt att aag aca acc ctt gaa gac atg gta aaa cat ggt gct aac ttg      576
Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu
            180                 185                 190

att cgt ttg gat gcc ttt gcg tat gca gtt aaa aaa gtt gac aca aat      624
Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn
        195                 200                 205

gac ttc ttc gtt gag cca gaa atc tgg gac act ttg aat gaa gta cgt      672
Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg
    210                 215                 220

gaa att ttg aca cca tta aag gct gaa att tta cca gaa att cat gaa      720
Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu
225                 230                 235                 240

cat tac tca atc cct aaa aag atc aat gat cat ggt tac ttc acc tat      768
His Tyr Ser Ile Pro Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr
                245                 250                 255

gac ttt gca tta cca atg aca acg ctt tac aca ttg tat tca ggt aag      816
Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys
            260                 265                 270

aca aat caa ttg gca aag tgg ttg aag atg tca cca atg aag caa ttc      864
Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe
        275                 280                 285

aca aca ttg gac acg cat gat ggt att ggt gtc gtt gat gcc cgt gat      912
Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
    290                 295                 300

att cta act gat gat gaa att gac tac gct tct gaa caa ctt tac aag      960
Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys
305                 310                 315                 320

gtt ggc gcg aat gtc aaa aag aca tat tca tct gct tca tac aac aac     1008
Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn
                325                 330                 335

ctt gat att tac caa att aac tca act tat tat tca gca ttg gga aat     1056
Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
            340                 345                 350

gat gat gca gca tac ttg ttg agt cgt gtc ttc caa gtc ttt gcg cct     1104
Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
        355                 360                 365

gga att cca caa att tat tac gtt ggt ttg ttg gca ggt gaa aac gat     1152
Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
    370                 375                 380

atc gcg ctt ttg gag tca act aaa gaa ggt cgt aat att aac cgt cat     1200
Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His
385                 390                 395                 400

tac tat acg cgt gaa gaa gtt aag tca gaa gtt aag cga cca gtt gtt     1248
Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val
                405                 410                 415

gct aac tta ttg aag cta ttg tca tgg cgt aat gaa agc cct gca ttt     1296
Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe
            420                 425                 430
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```
gat ttg gct ggc tca atc aca gtt gac acg cca act gat aca aca att      1344
Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
        435                 440                 445

gtg gtg aca cgt caa gat gaa aat ggt caa aac aaa gct gta tta aca      1392
Val Val Thr Arg Gln Asp Glu Asn Gly Gln Asn Lys Ala Val Leu Thr
    450                 455                 460

gcc gat gcg gcc aac aaa act ttt gaa atc gtt gag aat ggt caa act      1440
Ala Asp Ala Ala Asn Lys Thr Phe Glu Ile Val Glu Asn Gly Gln Thr
465                 470                 475                 480

gtt atg agc agt gat aat ttg act cag aac                              1470
Val Met Ser Ser Asp Asn Leu Thr Gln Asn
                485                 490
```

<210> 8
<211> 490
<212> PRT
<213> Leuconostoc mesenteroides

<400> 8

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Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                   10                  15

Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly
            20                  25                  30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe
    50                  55                  60

Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln
                85                  90                  95

Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile
            100                 105                 110

Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln
        115                 120                 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln
    130                 135                 140

Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe
145                 150                 155                 160

Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu
                165                 170                 175

Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu
            180                 185                 190

Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn
        195                 200                 205

Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg
    210                 215                 220

Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu
225                 230                 235                 240
```

```
His Tyr Ser Ile Pro Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr
                245                 250                 255

Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys
            260                 265                 270

Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe
        275                 280                 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
    290                 295                 300

Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys
305                 310                 315                 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn
                325                 330                 335

Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
            340                 345                 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
        355                 360                 365

Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
    370                 375                 380

Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His
385                 390                 395                 400

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val
                405                 410                 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe
            420                 425                 430

Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
        435                 440                 445

Val Val Thr Arg Gln Asp Glu Asn Gly Gln Asn Lys Ala Val Leu Thr
    450                 455                 460

Ala Asp Ala Ala Asn Lys Thr Phe Glu Ile Val Glu Asn Gly Gln Thr
465                 470                 475                 480

Val Met Ser Ser Asp Asn Leu Thr Gln Asn
                485                 490
```

<210> 9
<211> 1467
<212> DNA
<213> Oenococcus oeni

<220>
<221> CDS
<222> (1)..(1467)

<400> 9

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atg ccg gtt aaa aat aaa gca atg ctg atc acc tat tcg gat tcg atg      48
Met Pro Val Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Met
1               5                   10                  15

ggt aag aat atc aag gaa tta caa tac att tta gat aaa tat att gga      96
Gly Lys Asn Ile Lys Glu Leu Gln Tyr Ile Leu Asp Lys Tyr Ile Gly
            20                  25                  30

gac gcg att ggt gga gtt cat ctg ctg cct ttt ttt ccg tca acc gga     144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
```

```
        35                  40                  45

gat cgt ggt ttt gcg ccc tcg gat tac act cgt gtc aat ccg gat ttc      192
Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asn Pro Asp Phe
    50                  55                  60

ggt gat tgg gag gat gtc gag gaa ctt gga aaa aag tat tat tta atg      240
Gly Asp Trp Glu Asp Val Glu Glu Leu Gly Lys Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttc atg att aat cac att tcc cgt gaa tcg att atg tat caa      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Ile Met Tyr Gln
                85                  90                  95

gat ttc aag gaa aaa aag gat gct tcc agc tac aag gac ttt ttt att      336
Asp Phe Lys Glu Lys Lys Asp Ala Ser Ser Tyr Lys Asp Phe Phe Ile
            100                 105                 110

cgt tgg gaa aag ttc tgg ccg aaa gga cgc ccg acg aag gcc gat atc      384
Arg Trp Glu Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Ala Asp Ile
        115                 120                 125

gat tta att tac aaa aga aaa gat aag gcg ccg att cag ggg att act      432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln Gly Ile Thr
    130                 135                 140

ttt gca gac ggc agt caa gaa cat ctt tgg aat act ttt ggc gat gag      480
Phe Ala Asp Gly Ser Gln Glu His Leu Trp Asn Thr Phe Gly Asp Glu
145                 150                 155                 160

cag atc gat att aac gtg aag tcc aaa gtt gct cag gaa ttt ttt aaa      528
Gln Ile Asp Ile Asn Val Lys Ser Lys Val Ala Gln Glu Phe Phe Lys
                165                 170                 175

gat act tta cag tca atg gtt aag cac ggt gcg gat ttg att cgc ctg      576
Asp Thr Leu Gln Ser Met Val Lys His Gly Ala Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gct tat gca att aaa aag att gat act aat gac ttc ttt      624
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Ile Asp Thr Asn Asp Phe Phe
        195                 200                 205

att gaa ccg gaa att tgg gat tta ctg gaa tca gtt cgg aag att ctc      672
Ile Glu Pro Glu Ile Trp Asp Leu Leu Glu Ser Val Arg Lys Ile Leu
    210                 215                 220

gac ccc cta cat gct gaa att tta ccg gaa att tat gaa cat tac aca      720
Asp Pro Leu His Ala Glu Ile Leu Pro Glu Ile Tyr Glu His Tyr Thr
225                 230                 235                 240

atc ccg gcc aaa ata aat gag tat ggt tac ttt acc tat gat ttt gtt      768
Ile Pro Ala Lys Ile Asn Glu Tyr Gly Tyr Phe Thr Tyr Asp Phe Val
                245                 250                 255

tta cct ctg gta att ttg tac act ctt tat tct gga aat ccc aag caa      816
Leu Pro Leu Val Ile Leu Tyr Thr Leu Tyr Ser Gly Asn Pro Lys Gln
            260                 265                 270

ttg gcc aaa tgg ttg aaa atg tca cca aaa aaa cag ttt acg act ctt      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat act cat gat gga atc ggg gtt gtt gat gct cgc gat att tta act      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Thr
    290                 295                 300

gat gag gaa atc gac tat act tcc agt gaa ctg tat aaa gtt ggt gcg      960
Asp Glu Glu Ile Asp Tyr Thr Ser Ser Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aac gtc aaa cgg act tat tca tct gcg gcc tat aat aat ttg gat att     1008
Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tac cag att aac tcg acc tat tat tca gct ctt ggc aat gat gac aaa     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

gcc tat ttg ctt gcc cgt gca ata caa att ttt gcc ccg gga att cca     1104
Ala Tyr Leu Leu Ala Arg Ala Ile Gln Ile Phe Ala Pro Gly Ile Pro
        355                 360                 365

caa atc tat tac gca ggc ctg ctg gct ggt gaa aac gat ttg gat ttg     1152
Gln Ile Tyr Tyr Ala Gly Leu Leu Ala Gly Glu Asn Asp Leu Asp Leu
    370                 375                 380
```

```
ttg gaa aag acc aag gaa gga cgc aat ata aat cgt cat tat tac agt      1200
Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

gaa gaa gaa gtt gcc aat gaa gtg cag aga cca att gtt gcc tgc cta      1248
Glu Glu Glu Val Ala Asn Glu Val Gln Arg Pro Ile Val Ala Cys Leu
                405                 410                 415

ctg aaa ttg ttg gct tgg cgc aat cgc agt gcc gct ttt gat ctt caa      1296
Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gln
            420                 425                 430

gga gat att caa gtc agc gca acc gac aaa aat gaa atc aaa att att      1344
Gly Asp Ile Gln Val Ser Ala Thr Asp Lys Asn Glu Ile Lys Ile Ile
        435                 440                 445

cga act tca acc aat ggc caa gac acc gcg gaa tta acc gct aat gtg      1392
Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val
    450                 455                 460

gct cta aaa acc ttt act ata aag gaa aat gat aaa att att tta att      1440
Ala Leu Lys Thr Phe Thr Ile Lys Glu Asn Asp Lys Ile Ile Leu Ile
465                 470                 475                 480

gaa gat cag act gat aca aag gat atc                                 1467
Glu Asp Gln Thr Asp Thr Lys Asp Ile
                485
```

<210> 10
<211> 489
<212> PRT
<213> Oenococcus oeni

<400> 10

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Met Pro Val Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Met
1               5                   10                  15

Gly Lys Asn Ile Lys Glu Leu Gln Tyr Ile Leu Asp Lys Tyr Ile Gly
            20                  25                  30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asn Pro Asp Phe
    50                  55                  60

Gly Asp Trp Glu Asp Val Glu Glu Leu Gly Lys Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Ile Met Tyr Gln
                85                  90                  95

Asp Phe Lys Glu Lys Lys Asp Ala Ser Ser Tyr Lys Asp Phe Phe Ile
            100                 105                 110

Arg Trp Glu Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Ala Asp Ile
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln Gly Ile Thr
    130                 135                 140

Phe Ala Asp Gly Ser Gln Glu His Leu Trp Asn Thr Phe Gly Asp Glu
145                 150                 155                 160

Gln Ile Asp Ile Asn Val Lys Ser Lys Val Ala Gln Glu Phe Phe Lys
                165                 170                 175

Asp Thr Leu Gln Ser Met Val Lys His Gly Ala Asp Leu Ile Arg Leu
            180                 185                 190
```

```
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Ile Asp Thr Asn Asp Phe Phe
        195                 200                 205

Ile Glu Pro Glu Ile Trp Asp Leu Leu Glu Ser Val Arg Lys Ile Leu
    210                 215                 220

Asp Pro Leu His Ala Glu Ile Leu Pro Glu Ile Tyr Glu His Tyr Thr
225                 230                 235                 240

Ile Pro Ala Lys Ile Asn Glu Tyr Gly Tyr Phe Thr Tyr Asp Phe Val
                245                 250                 255

Leu Pro Leu Val Ile Leu Tyr Thr Leu Tyr Ser Gly Asn Pro Lys Gln
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Asp Tyr Thr Ser Ser Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

Ala Tyr Leu Leu Ala Arg Ala Ile Gln Ile Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Ile Tyr Tyr Ala Gly Leu Leu Ala Gly Glu Asn Asp Leu Asp Leu
    370                 375                 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Glu Glu Glu Val Ala Asn Glu Val Gln Arg Pro Ile Val Ala Cys Leu
                405                 410                 415

Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gln
            420                 425                 430

Gly Asp Ile Gln Val Ser Ala Thr Asp Lys Asn Glu Ile Lys Ile Ile
        435                 440                 445

Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val
    450                 455                 460

Ala Leu Lys Thr Phe Thr Ile Lys Glu Asn Asp Lys Ile Ile Leu Ile
465                 470                 475                 480

Glu Asp Gln Thr Asp Thr Lys Asp Ile
                485
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<210> 11
<211> 1446
<212> DNA
<213> Streptococcus mitis

<220>
<221> CDS
<222> (1)..(1446)

<400> 11

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atg cca att cag aat aaa acc atg ttg att acc tat tca gat agt ctg       48
Met Pro Ile Gln Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu
1               5                  10                  15

gga aat aat ctt aaa gac tta tat gag aat ttg gaa gag tat ttt gga       96
Gly Asn Asn Leu Lys Asp Leu Tyr Glu Asn Leu Glu Glu Tyr Phe Gly
            20                  25                  30

gat gct att ggg gga gtt cac ctt cta cca ttt ttc cca tca aca ggt      144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gat tca gct ttt      192
Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
    50                  55                  60

ggt gat tgg gag gat gtt aag cgt tta ggt gag aaa tat tat ctt atg      240
Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gac ttt atg att aat cat att tct cgt caa tct aag tat tat aag      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gat ctc ttt tta      336
Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Asp Leu Phe Leu
            100                 105                 110

aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta      384
Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
        115                 120                 125

gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtt      432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
    130                 135                 140

ttt gaa gat ggg tca gtc gaa cat ttg tgg aat acc ttt ggt gag gag      480
Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

cag att gat ctt gat gtg acc aaa gaa gta act atg gaa ttt atc cgt      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
                165                 170                 175

aag acc att cag cac ttg gca agt aat ggg tgt gat ttg att cgt cta      576
Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gac gcc ttt gct tat gca gtg aag aaa ttg gat act aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gta gaa cca gat att tgg gat tta ttg gac aaa gtt cga gat atc gct      672
Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

gct gag tat ggg aca gag ctc tta cct gag att cat gaa cat tat tcg      720
Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

att cag ttt aaa ata gca gac cat gat tac tat gtt tat gat ttt gct      768
Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

ctt cca atg gtg aca ctt tat act ctt tac agt tcc aga aca gag cgt      816
Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
            260                 265                 270

ttg gct aag tgg tta aag atg agc cca atg aag caa ttt acg acg cta      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gac acc cat gat ggg att gga gtg gtg gat gtc aag gat atc ttg aca      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

gat gag gag att gac tat gct tca aat gaa ctc tat aag gtt gga gct      960
Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtc aaa cgt aag tac tcc agt gcc gag tat aat aat tta gat atc     1008
Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335
```

```
tac caa atc aat tca acc tat tat tct gcg ctt gga gat gat gat gtc      1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
            340                 345                 350

aag tat ttc ctt gca cga tta att caa gca ttt gct cca ggt att cct      1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

caa gtt tac tat gta ggt cta tta gca ggc aag aat gat ttg aaa tta      1152
Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
    370                 375                 380

tta gaa gaa act aaa gta ggt cga aat att aat cgt cat tac tat agc      1200
Leu Glu Glu Thr Lys Val Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

aat gag gaa ata gca gaa gaa gtc caa cgt cct gta gtg aag gcc ctt      1248
Asn Glu Glu Ile Ala Glu Glu Val Gln Arg Pro Val Val Lys Ala Leu
                405                 410                 415

ctc aat cta ttt tct ttc cgt aat cga tca gta gca ttt gat tta gaa      1296
Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu
            420                 425                 430

gga act att gac gtt gaa aca cca aca gcc cac agc att gta atc aaa      1344
Gly Thr Ile Asp Val Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
        435                 440                 445

cgt caa aat aaa gat aag tcc gta aca gca gta gca gaa att gat ttg      1392
Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Ala Glu Ile Asp Leu
    450                 455                 460

caa aat cag act tat cga gta atg aga acg gaa tgg aag tac att ttg      1440
Gln Asn Gln Thr Tyr Arg Val Met Arg Thr Glu Trp Lys Tyr Ile Leu
465                 470                 475                 480

aag act                                                             1446
Lys Thr
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<210> 12
<211> 482
<212> PRT
<213> Streptococcus mitis

<400> 12

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Met Pro Ile Gln Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu
1               5                   10                  15

Gly Asn Asn Leu Lys Asp Leu Tyr Glu Asn Leu Glu Glu Tyr Phe Gly
            20                  25                  30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
    50                  55                  60

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Asp Leu Phe Leu
            100                 105                 110

Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
    130                 135                 140
```

```
Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
                165                 170                 175

Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
            340                 345                 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
    370                 375                 380

Leu Glu Glu Thr Lys Val Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Asn Glu Glu Ile Ala Glu Glu Val Gln Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu
            420                 425                 430

Gly Thr Ile Asp Val Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
        435                 440                 445

Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Ala Glu Ile Asp Leu
    450                 455                 460

Gln Asn Gln Thr Tyr Arg Val Met Arg Thr Glu Trp Lys Tyr Ile Leu
465                 470                 475                 480

Lys Thr
```

<210> 13
<211> 1458
<212> DNA
<213> Leuconostoc mesenteroides

<220>
<221> CDS
<222> (1)..(1458)

<400> 13

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atg gaa att caa aac aaa gca atg ctc att acg tat gct gat tct ttg       48
Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                  10                  15

ggc agt aat atc aag gaa gtc cac caa gtt ttg aag gaa gac att ggc       96
Gly Ser Asn Ile Lys Glu Val His Gln Val Leu Lys Glu Asp Ile Gly
            20                  25                  30

gat gcg att ggc ggg gta cat ttg tta cca ttt ttc cct tct aca ggt      144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat cgt ggc ttc gcc cct tct gat tac acg cgt gtt gat gca aca ttt      192
Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asp Ala Thr Phe
    50                  55                  60

ggt gat tgg aat gat gtt gag gca ctt ggg caa gaa tac tat ttg atg      240
Gly Asp Trp Asn Asp Val Glu Ala Leu Gly Gln Glu Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttt atg atc aat cat att tct cgt gaa tcg gag atg tat caa      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Glu Met Tyr Gln
                85                  90                  95

gat ttt aaa gca aat cac gat caa tca aag tac cgt gat ttc ttc att      336
Asp Phe Lys Ala Asn His Asp Gln Ser Lys Tyr Arg Asp Phe Phe Ile
            100                 105                 110

cgc tgg gaa aag ttt tgg caa cag gct ggg cca gat cga cca act caa      384
Arg Trp Glu Lys Phe Trp Gln Gln Ala Gly Pro Asp Arg Pro Thr Gln
        115                 120                 125

gca gac gtc gac ctt att tat aag cgc aaa gac aag gcg cca att caa      432
Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln
    130                 135                 140

gaa atc act ttt gct gac ggt acg aca gag cat ctt tgg aat aca ttt      480
Glu Ile Thr Phe Ala Asp Gly Thr Thr Glu His Leu Trp Asn Thr Phe
145                 150                 155                 160

ggt gaa gaa caa att gat att gat gtt aat tct caa att gct aaa gcc      528
Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Gln Ile Ala Lys Ala
                165                 170                 175

ttc att aaa gca acg cta gaa gac atg gtc caa cat ggt gcc aat ttg      576
Phe Ile Lys Ala Thr Leu Glu Asp Met Val Gln His Gly Ala Asn Leu
            180                 185                 190

att cgt tta gat gct ttc gcc tat gct gtt aag aaa gtt ggg aca aat      624
Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn
        195                 200                 205

gat ttc ttt gtc gaa cca gaa ata tgg act gtt tta aac gaa gtg cgt      672
Asp Phe Phe Val Glu Pro Glu Ile Trp Thr Val Leu Asn Glu Val Arg
    210                 215                 220

gac att ttg gca cct atg cat gct gaa att tta cca gaa att cat gag      720
Asp Ile Leu Ala Pro Met His Ala Glu Ile Leu Pro Glu Ile His Glu
225                 230                 235                 240

cat tat aca att cct caa aag atc aac gcc cat ggt tat ttc act tat      768
His Tyr Thr Ile Pro Gln Lys Ile Asn Ala His Gly Tyr Phe Thr Tyr
                245                 250                 255

gat ttt gct ttg cca atg aca gta ctt tat acg ctt tac tca ggc aaa      816
Asp Phe Ala Leu Pro Met Thr Val Leu Tyr Thr Leu Tyr Ser Gly Lys
            260                 265                 270

aca aat cga cta gcc aac tgg ctc aaa cag tct ccg atg aaa caa ttc      864
Thr Asn Arg Leu Ala Asn Trp Leu Lys Gln Ser Pro Met Lys Gln Phe
        275                 280                 285
```

```
acg acg tta gat acg cat gat ggc att ggg gtt gtt gac gca cgt gat      912
Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
    290                 295                 300

att ttg aca gac gaa gaa att gat tat gct tct gag gaa tta tac aaa      960
Ile Leu Thr Asp Glu Glu Ile Asp Tyr Ala Ser Glu Glu Leu Tyr Lys
305                 310                 315                 320

gtt gga gcc aat gtc aaa aag acc tac tca tca gct gcg tat aat aac     1008
Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn
                325                 330                 335

tta gat att tat cag att aat tca act tac tat tca gct tta ggc aat     1056
Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
            340                 345                 350

gat gat gcc gca tat ttg ttg agt cgt gtt ttc caa gtc ttt gca cct     1104
Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
        355                 360                 365

ggt att cca caa att tat tat gtc ggg tta ctt gca ggt gag aat gat     1152
Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
    370                 375                 380

att gat ttg ttg gaa tct tca aaa gaa ggt cgt aat att aat cgt cat     1200
Ile Asp Leu Leu Glu Ser Ser Lys Glu Gly Arg Asn Ile Asn Arg His
385                 390                 395                 400

tac tat act cgt gaa gaa ata aaa tca gct gtt aag cgg cca gtt gtt     1248
Tyr Tyr Thr Arg Glu Glu Ile Lys Ser Ala Val Lys Arg Pro Val Val
                405                 410                 415

gct gac tta ttg gca tta tta tca tgg cgt aat cag ttt tca gca ttt     1296
Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gln Phe Ser Ala Phe
            420                 425                 430

gct ctg gat ggg aca atc act gtc gag aca cca tca gaa cat gat att     1344
Ala Leu Asp Gly Thr Ile Thr Val Glu Thr Pro Ser Glu His Asp Ile
        435                 440                 445

aaa att aca cga acg gat cat tcc gga gat aat ata gct att ttg cta     1392
Lys Ile Thr Arg Thr Asp His Ser Gly Asp Asn Ile Ala Ile Leu Leu
    450                 455                 460

gct aat gcc aag aca cgc acc ttt gtc atc aca gca aat ggc aag aca     1440
Ala Asn Ala Lys Thr Arg Thr Phe Val Ile Thr Ala Asn Gly Lys Thr
465                 470                 475                 480

gtc tta caa aac aaa taa                                            1458
Val Leu Gln Asn Lys
                485
```

<210> 14
<211> 485
<212> PRT
<213> Leuconostoc mesenteroides

<400> 14

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Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                   10                  15

Gly Ser Asn Ile Lys Glu Val His Gln Val Leu Lys Glu Asp Ile Gly
            20                  25                  30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asp Ala Thr Phe
    50                  55                  60

Gly Asp Trp Asn Asp Val Glu Ala Leu Gly Gln Glu Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Glu Met Tyr Gln
                85                  90                  95
```

```
Asp Phe Lys Ala Asn His Asp Gln Ser Lys Tyr Arg Asp Phe Phe Ile
            100                 105                 110

Arg Trp Glu Lys Phe Trp Gln Gln Ala Gly Pro Asp Arg Pro Thr Gln
        115                 120                 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln
    130                 135                 140

Glu Ile Thr Phe Ala Asp Gly Thr Thr Glu His Leu Trp Asn Thr Phe
145                 150                 155                 160

Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Gln Ile Ala Lys Ala
                165                 170                 175

Phe Ile Lys Ala Thr Leu Glu Asp Met Val Gln His Gly Ala Asn Leu
            180                 185                 190

Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn
        195                 200                 205

Asp Phe Phe Val Glu Pro Glu Ile Trp Thr Val Leu Asn Glu Val Arg
    210                 215                 220

Asp Ile Leu Ala Pro Met His Ala Glu Ile Leu Pro Glu Ile His Glu
225                 230                 235                 240

His Tyr Thr Ile Pro Gln Lys Ile Asn Ala His Gly Tyr Phe Thr Tyr
                245                 250                 255

Asp Phe Ala Leu Pro Met Thr Val Leu Tyr Thr Leu Tyr Ser Gly Lys
            260                 265                 270

Thr Asn Arg Leu Ala Asn Trp Leu Lys Gln Ser Pro Met Lys Gln Phe
        275                 280                 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
    290                 295                 300

Ile Leu Thr Asp Glu Glu Ile Asp Tyr Ala Ser Glu Glu Leu Tyr Lys
305                 310                 315                 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn
                325                 330                 335

Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
            340                 345                 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
        355                 360                 365

Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
    370                 375                 380

Ile Asp Leu Leu Glu Ser Ser Lys Glu Gly Arg Asn Ile Asn Arg His
385                 390                 395                 400

Tyr Tyr Thr Arg Glu Glu Ile Lys Ser Ala Val Lys Arg Pro Val Val
                405                 410                 415

Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gln Phe Ser Ala Phe
            420                 425                 430

Ala Leu Asp Gly Thr Ile Thr Val Glu Thr Pro Ser Glu His Asp Ile
```

```
        435                 440                 445

Lys Ile Thr Arg Thr Asp His Ser Gly Asp Asn Ile Ala Ile Leu Leu
    450                 455                 460

Ala Asn Ala Lys Thr Arg Thr Phe Val Ile Thr Ala Asn Gly Lys Thr
465                 470                 475                 480

Val Leu Gln Asn Lys
                485
```

<210> 15
<211> 1443
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> CDS
<222> (1)..(1443)

<400> 15

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atg aaa tta caa aat aag gca ata ttg ata act tat cca gat agt tta       48
Met Lys Leu Gln Asn Lys Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu
1               5                  10                  15

ggt cat aat ttg aag gac ttg gat cat gta atg gat cgc tat ttt aat       96
Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn
            20                  25                  30

aaa acg ata ggt ggt att cat tta tta cca ttt ttc cct tca aac ggt      144
Lys Thr Ile Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Asn Gly
        35                  40                  45

gat cgc ggt ttt tct cct aca aga tat gat gta gtt gag cct aag ttt      192
Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
    50                  55                  60

ggt tca tgg gaa gat gta gaa aag tta agt caa aag tat tat ttg atg      240
Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gac ttt atg att aat cat ctt tct aaa aaa tcc tca tat ttt gaa      288
Phe Asp Phe Met Ile Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu
                85                  90                  95

gat ttt gaa gcc aag cac gat aaa agc aaa tat agc gat ctt ttc tta      336
Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu
            100                 105                 110

agt tgg gat aaa ttt tgg cca aag ggc aga cca act aaa gaa gat ata      384
Ser Trp Asp Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile
        115                 120                 125

gat tta att tat aaa cga aaa gat aag gcc cca tat caa aat att aaa      432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys
    130                 135                 140

ttt gaa gat ggt act cat gaa aag atg tgg aat act ttc ggc cca gat      480
Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp
145                 150                 155                 160

caa atg gat ttg gat gtt aga acc aag aca aca caa gat ttt ata aag      528
Gln Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys
                165                 170                 175

cat aat tta caa aat ctt tct aaa cat ggt gct agt ttg att cgt tta      576
His Asn Leu Gln Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu
            180                 185                 190

gat gca ttt gct tat gca att aaa aag tta gat aca aat gac ttc ttt      624
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gta gaa ccg gaa att tgg aat tta ctc gaa aag gta aat gat tat ctt      672
Val Glu Pro Glu Ile Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu
    210                 215                 220

aaa gat act cca act act att ctg cct gaa att cat gag cat tat acg      720
Lys Asp Thr Pro Thr Thr Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240
```

```
atg cca ttt aag gtg gca gaa cat gga tac ttt att tat gat ttt gct      768
Met Pro Phe Lys Val Ala Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala
                245                 250                 255

tta cca atg gta ttg ttg tat tca ctt tat agc ggt aat agt act caa      816
Leu Pro Met Val Leu Leu Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln
            260                 265                 270

ctt gct gct tgg cta aag aaa tgt ccg atg aag caa ttt act act tta      864
Leu Ala Ala Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat acc cac gat gga tta ggc gta gtt gac gca aag gat att ctt acg      912
Asp Thr His Asp Gly Leu Gly Val Val Asp Ala Lys Asp Ile Leu Thr
    290                 295                 300

gac gat caa att agc tac aca aca aac gaa ctt tat aaa att ggt gct      960
Asp Asp Gln Ile Ser Tyr Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala
305                 310                 315                 320

aac gtc aag aag aaa tat tct agt gct gaa tat cat aat ttg gat att     1008
Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
                325                 330                 335

tat caa att aat act act tat tat tct gca ttg ggt aat gat gat aaa     1056
Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

aaa tat ttt att gca cgg tta tta caa atc ttt gcc cct ggt att cca     1104
Lys Tyr Phe Ile Ala Arg Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro
        355                 360                 365

caa att tat tat gtt gga ttg tta gca gga gaa aat gat att caa tta     1152
Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu
    370                 375                 380

tta gag aag aca aaa gaa gga cgc gat att aat cgc cac tat tat gat     1200
Leu Glu Lys Thr Lys Glu Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp
385                 390                 395                 400

ttg gat gag att gcg gaa caa gtt caa aga cct gta gta aaa tct ttg     1248
Leu Asp Glu Ile Ala Glu Gln Val Gln Arg Pro Val Val Lys Ser Leu
                405                 410                 415

att aag tta ttg gaa ttt cgt aat tct gta cct gca ttt gat ttg gaa     1296
Ile Lys Leu Leu Glu Phe Arg Asn Ser Val Pro Ala Phe Asp Leu Glu
            420                 425                 430

ggt tca atc aaa gtt gaa act cca agt gaa cat gaa att att gtc act     1344
Gly Ser Ile Lys Val Glu Thr Pro Ser Glu His Glu Ile Ile Val Thr
        435                 440                 445

aga tca aat aag gca gga aca gaa gta gct agt acg tac gta gac ttt     1392
Arg Ser Asn Lys Ala Gly Thr Glu Val Ala Ser Thr Tyr Val Asp Phe
    450                 455                 460

aag aac tta gac tat caa gtt aaa tac aat gat cag gtc ttt aat ttt     1440
Lys Asn Leu Asp Tyr Gln Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
465                 470                 475                 480

tag                                                                1443
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<210> 16
<211> 480
<212> PRT
<213> Lactobacillus acidophilus

<400> 16

```
Met Lys Leu Gln Asn Lys Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu
1               5                   10                  15

Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn
            20                  25                  30

Lys Thr Ile Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Asn Gly
        35                  40                  45

Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
    50                  55                  60
```

```
Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu
                85                  90                  95

Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu
            100                 105                 110

Ser Trp Asp Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys
    130                 135                 140

Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp
145                 150                 155                 160

Gln Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys
                165                 170                 175

His Asn Leu Gln Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu
    210                 215                 220

Lys Asp Thr Pro Thr Thr Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

Met Pro Phe Lys Val Ala Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Leu Leu Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln
            260                 265                 270

Leu Ala Ala Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Leu Gly Val Val Asp Ala Lys Asp Ile Leu Thr
    290                 295                 300

Asp Asp Gln Ile Ser Tyr Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala
305                 310                 315                 320

Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

Lys Tyr Phe Ile Ala Arg Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu
    370                 375                 380

Leu Glu Lys Thr Lys Glu Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp
385                 390                 395                 400
```

```
Leu Asp Glu Ile Ala Glu Gln Val Gln Arg Pro Val Val Lys Ser Leu
                405                 410                 415

Ile Lys Leu Leu Glu Phe Arg Asn Ser Val Pro Ala Phe Asp Leu Glu
            420                 425                 430

Gly Ser Ile Lys Val Glu Thr Pro Ser Glu His Glu Ile Ile Val Thr
        435                 440                 445

Arg Ser Asn Lys Ala Gly Thr Glu Val Ala Ser Thr Tyr Val Asp Phe
    450                 455                 460

Lys Asn Leu Asp Tyr Gln Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
465                 470                 475                 480
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<210> 17
<211> 1443
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> CDS
<222> (1)..(1443)

<400> 17

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atg cca att gaa aat aaa gta atg tta att act tat cca gac agt ttg      48
Met Pro Ile Glu Asn Lys Val Met Leu Ile Thr Tyr Pro Asp Ser Leu
1               5                   10                  15

ggt aaa aat tta aaa gaa tta gat gaa att tta agt gaa gac ttg aag      96
Gly Lys Asn Leu Lys Glu Leu Asp Glu Ile Leu Ser Glu Asp Leu Lys
            20                  25                  30

ggg gct gta ggc ggt att cac tta ttg cca ttc ttc cca tca act ggt     144
Gly Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gac cgt gga ttt gct ccg act gga tat aca gaa gta gat cct aag ttt     192
Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe
    50                  55                  60

ggt gat tgg tca gac att gaa aaa ata ggt aag aaa tat tat ttg atg     240
Gly Asp Trp Ser Asp Ile Glu Lys Ile Gly Lys Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttt atg att aat cat att tct cgt caa tca aaa ttt tat aaa     288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Phe Tyr Lys
                85                  90                  95

gat ttc aaa caa aag aaa gat aaa agt aag tat gcc gat tta ttt ttg     336
Asp Phe Lys Gln Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu
            100                 105                 110

agc tgg gac aaa ttt tgg ccg gaa ggt cgt cca act cga aaa gat att     384
Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile
        115                 120                 125

gat tta att tat aaa cga aaa gat cgt gct cca tat caa gaa att act     432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gln Glu Ile Thr
    130                 135                 140

ttt aca gat ggc agt aaa gaa aaa tta tgg aat act ttt ggt gaa gag     480
Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

caa atc gat atg gat gtt cga aag gag gtg aca cag aag ttt att aaa     528
Gln Ile Asp Met Asp Val Arg Lys Glu Val Thr Gln Lys Phe Ile Lys
                165                 170                 175

gat acg ttg aga gca tta att gat cat ggt gct gat att att cgg tta     576
Asp Thr Leu Arg Ala Leu Ile Asp His Gly Ala Asp Ile Ile Arg Leu
            180                 185                 190

gat gct ttt gcg tat gct gta aag aag tta gat act aat gat ttc ttt     624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gta gag cca gaa att tgg gat tta cta aaa caa gta caa gat gat att     672
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Val Glu Pro Glu Ile Trp Asp Leu Leu Lys Gln Val Gln Asp Asp Ile
    210                 215                 220

tct gat aaa ggt gca atg att cta cca gaa ata cat gaa cac tat tca      720
Ser Asp Lys Gly Ala Met Ile Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

atg cca ttt aag att tca aag cat gga tat tat atc tat gac ttt gct      768
Met Pro Phe Lys Ile Ser Lys His Gly Tyr Tyr Ile Tyr Asp Phe Ala
                245                 250                 255

tta cca atg gta act tta tat tca ctt tat tca ggt aag tcc aat cgc      816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Ser Asn Arg
            260                 265                 270

tta gct gat tgg ctt aag aaa tgt cca atg aaa cag ttc act acc tta      864
Leu Ala Asp Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat aca cat gat ggt atc ggt gtt gtt gat gct cgt gat att ctc tcc      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Ser
    290                 295                 300

cct gac gaa att aaa tac aca agt aat gaa ttg tat aaa gtt gga gct      960
Pro Asp Glu Ile Lys Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtt aaa aag aaa tat tct agt gcc gaa tat cat aat tta gat atc     1008
Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
                325                 330                 335

tac caa att aat aca act tat tat tct gct tta ggc aat gat gat aaa     1056
Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

aaa tac ttt att gcg aga ctt att caa atg ttt gcg cct ggt att ccg     1104
Lys Tyr Phe Ile Ala Arg Leu Ile Gln Met Phe Ala Pro Gly Ile Pro
        355                 360                 365

caa gtc tat tat gta gga atg ctg gct ggt aaa aac gat atc gaa ctc     1152
Gln Val Tyr Tyr Val Gly Met Leu Ala Gly Lys Asn Asp Ile Glu Leu
    370                 375                 380

ctc gaa aag act aaa gaa ggt aga aac att aat cgt cat tac tat ggc     1200
Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Gly
385                 390                 395                 400

aga gaa gaa gta gct gaa gaa act aaa aga cct tta gta gca gca ctc     1248
Arg Glu Glu Val Ala Glu Glu Thr Lys Arg Pro Leu Val Ala Ala Leu
                405                 410                 415

ttg aaa ttg ttt aat ttt aga aac aat gaa gca gct ttt gat ctt gat     1296
Leu Lys Leu Phe Asn Phe Arg Asn Asn Glu Ala Ala Phe Asp Leu Asp
            420                 425                 430

gga tcc att gaa atc act acg cct aat gaa aac gtg att caa ata act     1344
Gly Ser Ile Glu Ile Thr Thr Pro Asn Glu Asn Val Ile Gln Ile Thr
        435                 440                 445

cgt atg aat aaa gat aaa act cga aaa gca aga gct gtt att aat tta     1392
Arg Met Asn Lys Asp Lys Thr Arg Lys Ala Arg Ala Val Ile Asn Leu
    450                 455                 460

aaa aat tta act tat caa gtg act gta aat aat gag gtt att aac ttt     1440
Lys Asn Leu Thr Tyr Gln Val Thr Val Asn Asn Glu Val Ile Asn Phe
465                 470                 475                 480

taa                                                                1443


<210> 18
<211> 480
<212> PRT
<213> Lactobacillus acidophilus

<400> 18

Met Pro Ile Glu Asn Lys Val Met Leu Ile Thr Tyr Pro Asp Ser Leu
1               5                   10                  15

Gly Lys Asn Leu Lys Glu Leu Asp Glu Ile Leu Ser Glu Asp Leu Lys
            20                  25                  30
```

```
Gly Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe
    50                  55                  60

Gly Asp Trp Ser Asp Ile Glu Lys Ile Gly Lys Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Phe Tyr Lys
                85                  90                  95

Asp Phe Lys Gln Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu
            100                 105                 110

Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gln Glu Ile Thr
    130                 135                 140

Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Met Asp Val Arg Lys Glu Val Thr Gln Lys Phe Ile Lys
                165                 170                 175

Asp Thr Leu Arg Ala Leu Ile Asp His Gly Ala Asp Ile Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Lys Gln Val Gln Asp Asp Ile
    210                 215                 220

Ser Asp Lys Gly Ala Met Ile Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

Met Pro Phe Lys Ile Ser Lys His Gly Tyr Tyr Ile Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Ser Asn Arg
            260                 265                 270

Leu Ala Asp Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Ser
    290                 295                 300

Pro Asp Glu Ile Lys Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
            340                 345                 350

Lys Tyr Phe Ile Ala Arg Leu Ile Gln Met Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Val Tyr Tyr Val Gly Met Leu Ala Gly Lys Asn Asp Ile Glu Leu
```

```
    370                 375                 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Gly
385                 390                 395                 400

Arg Glu Glu Val Ala Glu Glu Thr Lys Arg Pro Leu Val Ala Ala Leu
                405                 410                 415

Leu Lys Leu Phe Asn Phe Arg Asn Asn Glu Ala Ala Phe Asp Leu Asp
            420                 425                 430

Gly Ser Ile Glu Ile Thr Thr Pro Asn Glu Asn Val Ile Gln Ile Thr
        435                 440                 445

Arg Met Asn Lys Asp Lys Thr Arg Lys Ala Arg Ala Val Ile Asn Leu
    450                 455                 460

Lys Asn Leu Thr Tyr Gln Val Thr Val Asn Asn Glu Val Ile Asn Phe
465                 470                 475                 480
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<210> 19
<211> 1443
<212> DNA
<213> Listeria monocytogenes

<220>
<221> CDS
<222> (1)..(1443)

<400> 19

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atg caa att aaa aat aaa gct atg tta att act tat tct gat agt tta      48
Met Gln Ile Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Leu
1               5                   10                  15

ggg aaa aat atg gaa gaa tta tcc aag gtg atg gaa act tat ttt gaa      96
Gly Lys Asn Met Glu Glu Leu Ser Lys Val Met Glu Thr Tyr Phe Glu
            20                  25                  30

gat gct gtt ggc ggg att cac tta ttg ccg ttc ttt cca tcc act gga     144
Asp Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat cga ggg ttt gcg cca agt gat tac aca aca gta gat agc gac cta     192
Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Thr Val Asp Ser Asp Leu
    50                  55                  60

ggt tct tgg gaa ata atc gag aaa tta ggc gaa aag tat tat tta atg     240
Gly Ser Trp Glu Ile Ile Glu Lys Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

ttt gat ttt atg att aat cac att tct cgc gaa tca ctc ttc ttt caa     288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Leu Phe Phe Gln
                85                  90                  95

gat ttt aaa aaa gag cat tta aac tca aag tat aaa gat atg ttt att     336
Asp Phe Lys Lys Glu His Leu Asn Ser Lys Tyr Lys Asp Met Phe Ile
            100                 105                 110

cgt atc aat gat ttc ttt cct ccg ggt aga cca aat gaa aaa gac tta     384
Arg Ile Asn Asp Phe Phe Pro Pro Gly Arg Pro Asn Glu Lys Asp Leu
        115                 120                 125

gat tta att tat aag aga aaa gat aag gcg cct ttt caa gaa gtt gaa     432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Phe Gln Glu Val Glu
    130                 135                 140

ttt gct gat ggg gga acg gaa tta gtt tgg aat act ttt ggg gaa gaa     480
Phe Ala Asp Gly Gly Thr Glu Leu Val Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

caa att gat tta gat gtg aca gcc gaa gtt aca aaa gaa ttt att cgt     528
Gln Ile Asp Leu Asp Val Thr Ala Glu Val Thr Lys Glu Phe Ile Arg
                165                 170                 175

caa acg ata aaa aat atg gct gca cat ggt tgt tct att ttg cgt ctt     576
Gln Thr Ile Lys Asn Met Ala Ala His Gly Cys Ser Ile Leu Arg Leu
            180                 185                 190
```

```
gat gcc ttt gct tat gca att aaa aaa tta gat aca aat gat ttt ttt      624
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gta gaa ccg gaa att tgg gat tta ctg gat gaa gtg aaa gca gaa gcg      672
Val Glu Pro Glu Ile Trp Asp Leu Leu Asp Glu Val Lys Ala Glu Ala
    210                 215                 220

gcc aaa tat gac atg gaa tta tta cca gaa att cat gaa cat tat tcc      720
Ala Lys Tyr Asp Met Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

atc caa atg aaa atc gcg aac cat gat tat tat atc tat gat ttt gcg      768
Ile Gln Met Lys Ile Ala Asn His Asp Tyr Tyr Ile Tyr Asp Phe Ala
                245                 250                 255

tta ccc atg gtg atg ctg tac tcg tta tat agt ggc cga gtg gaa cgt      816
Leu Pro Met Val Met Leu Tyr Ser Leu Tyr Ser Gly Arg Val Glu Arg
            260                 265                 270

tta gct aaa tgg tta gaa atg agt ccg atg aag caa ttt act act tta      864
Leu Ala Lys Trp Leu Glu Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat acg cat gat ggc att ggc gtt gtg gat gca cgc gat tta tta aca      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Leu Leu Thr
    290                 295                 300

gat gag gaa ctc gat tat act tca gca gaa tta tac aaa ata gga gct      960
Asp Glu Glu Leu Asp Tyr Thr Ser Ala Glu Leu Tyr Lys Ile Gly Ala
305                 310                 315                 320

aat gtt aaa aag ata tat tcc tct gaa aaa tat aat aac ctg gat att     1008
Asn Val Lys Lys Ile Tyr Ser Ser Glu Lys Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tat caa att aat agt acc tat tat agt gct ttg ggt gac gat gat aaa     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
            340                 345                 350

agt tac ttg tta gcg aga gta att caa tgt ttt gcg ccg ggg att ccg     1104
Ser Tyr Leu Leu Ala Arg Val Ile Gln Cys Phe Ala Pro Gly Ile Pro
        355                 360                 365

caa att tat tat gtt ggt tta ctt gct ggc aaa aat gat att gac ctt     1152
Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Ile Asp Leu
    370                 375                 380

tta gag gaa aca aaa gaa ggg cgt aat att aat cgt cat tac tac aca     1200
Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Thr
385                 390                 395                 400

ata gat gaa att aaa aat gaa gta aaa aga cca gtt gtt aaa gcg ttg     1248
Ile Asp Glu Ile Lys Asn Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

tgc aat tta ctg agg ttt aga aat act tct gaa gcg ttt gat ttg gaa     1296
Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu
            420                 425                 430

gga agt ata gaa att gag aca cct agc tca aat gaa atc gtt att att     1344
Gly Ser Ile Glu Ile Glu Thr Pro Ser Ser Asn Glu Ile Val Ile Ile
        435                 440                 445

cgc aaa aac aaa aca aat aaa att aca gcg aca tta aaa gca aat tta     1392
Arg Lys Asn Lys Thr Asn Lys Ile Thr Ala Thr Leu Lys Ala Asn Leu
    450                 455                 460

agt act aaa aca ttc caa atc agc gaa aat gaa aga aat att tta att     1440
Ser Thr Lys Thr Phe Gln Ile Ser Glu Asn Glu Arg Asn Ile Leu Ile
465                 470                 475                 480

taa                                                                1443
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<210> 20
<211> 480
<212> PRT
<213> Listeria monocytogenes

<400> 20

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Met Gln Ile Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Leu
1               5                   10                  15
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Gly Lys Asn Met Glu Glu Leu Ser Lys Val Met Glu Thr Tyr Phe Glu
            20                  25                  30

Asp Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Thr Val Asp Ser Asp Leu
    50                  55                  60

Gly Ser Trp Glu Ile Ile Glu Lys Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Leu Phe Phe Gln
                85                  90                  95

Asp Phe Lys Lys Glu His Leu Asn Ser Lys Tyr Lys Asp Met Phe Ile
            100                 105                 110

Arg Ile Asn Asp Phe Phe Pro Pro Gly Arg Pro Asn Glu Lys Asp Leu
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Phe Gln Glu Val Glu
    130                 135                 140

Phe Ala Asp Gly Gly Thr Glu Leu Val Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Ala Glu Val Thr Lys Glu Phe Ile Arg
                165                 170                 175

Gln Thr Ile Lys Asn Met Ala Ala His Gly Cys Ser Ile Leu Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Asp Glu Val Lys Ala Glu Ala
    210                 215                 220

Ala Lys Tyr Asp Met Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225                 230                 235                 240

Ile Gln Met Lys Ile Ala Asn His Asp Tyr Tyr Ile Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Met Leu Tyr Ser Leu Tyr Ser Gly Arg Val Glu Arg
            260                 265                 270

Leu Ala Lys Trp Leu Glu Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Leu Leu Thr
    290                 295                 300

Asp Glu Glu Leu Asp Tyr Thr Ser Ala Glu Leu Tyr Lys Ile Gly Ala
305                 310                 315                 320

Asn Val Lys Lys Ile Tyr Ser Ser Glu Lys Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
            340                 345                 350
```

```
Ser Tyr Leu Leu Ala Arg Val Ile Gln Cys Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Ile Asp Leu
    370                 375                 380

Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Thr
385                 390                 395                 400

Ile Asp Glu Ile Lys Asn Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu
            420                 425                 430

Gly Ser Ile Glu Ile Glu Thr Pro Ser Ser Asn Glu Ile Val Ile Ile
        435                 440                 445

Arg Lys Asn Lys Thr Asn Lys Ile Thr Ala Thr Leu Lys Ala Asn Leu
    450                 455                 460

Ser Thr Lys Thr Phe Gln Ile Ser Glu Asn Glu Arg Asn Ile Leu Ile
465                 470                 475                 480
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<210> 21
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutant of Streptococcus mutans sucrose phyophorylase

<220>
<221> CDS
<222> (1)..(1443)

<400> 21

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atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg      48
Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                   10                  15

ggt aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga      96
Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
            20                  25                  30

gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc tca ggt     144
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly
        35                  40                  45

gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac cct gct ttt     192
Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Pro Ala Phe
    50                  55                  60

ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa cat tac ctc atg     240
Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met
65                  70                  75                  80

ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa     288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta     336
Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
            100                 105                 110

aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat ctg     384
Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Leu
        115                 120                 125

gac ctg att tat aag cgt aag gat cga gca cct atg cag gaa atc cga     432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Met Gln Glu Ile Arg
    130                 135                 140

ttt gca gat ggc agt gtt gaa cat ctc tgg agc act ttt ggg gag gaa     480
Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu
```

```
145                 150                 155                 160

cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
                165                 170                 175

tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg      576
Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct      672
Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act      720
Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

att caa ttt aaa att gca gac cat ggt tac tat gtt tat gat ttt gcc      768
Ile Gln Phe Lys Ile Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt      816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc      960
Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc     1008
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
            340                 345                 350

aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca     1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta     1152
Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
    370                 375                 380

ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt     1200
Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt     1248
Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat     1296
Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
            420                 425                 430

ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa     1344
Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
        435                 440                 445

cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc     1392
Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
    450                 455                 460

caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt     1440
Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe
465                 470                 475                 480

gaa                                                                1443
Glu
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<210> 22
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

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Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                  10                  15

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
            20                  25                  30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Pro Ala Phe
    50                  55                  60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
            100                 105                 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Leu
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Met Gln Glu Ile Arg
    130                 135                 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
                165                 170                 175

Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

Ile Gln Phe Lys Ile Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
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    290                 295                 300

Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
            340                 345                 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
    370                 375                 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
            420                 425                 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
        435                 440                 445

Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
    450                 455                 460

Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe
465                 470                 475                 480

Glu
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<210> 23
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutant of Streptococcus mutans sucrose phyophorylase

<220>
<221> CDS
<222> (1)..(1461)

<400> 23

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atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg      48
Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                   10                  15

ggt aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga      96
Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
            20                  25                  30

gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt     144
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt     192
Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
    50                  55                  60

ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg     240
Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80
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ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta      336
Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
            100                 105                 110

aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg      384
Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
        115                 120                 125

gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa      432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
    130                 135                 140

ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa      480
Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
                165                 170                 175

tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg      576
Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct      672
Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220

gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act      720
Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcc      768
Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt      816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc      960
Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc     1008
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa     1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
            340                 345                 350

aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca     1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta     1152
Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
    370                 375                 380

ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt     1200
Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt     1248
Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat     1296
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Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
            420                 425                 430

ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa      1344
Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
        435                 440                 445

cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc      1392
Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
    450                 455                 460

caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc tta      1440
Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Leu
465                 470                 475                 480

tcc atg ata agc tgt caa aca                                         1461
Ser Met Ile Ser Cys Gln Thr
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<210> 24
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1               5                   10                  15

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
            20                  25                  30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
        35                  40                  45

Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
    50                  55                  60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65                  70                  75                  80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
                85                  90                  95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
            100                 105                 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
        115                 120                 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
    130                 135                 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145                 150                 155                 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
                165                 170                 175

Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
            180                 185                 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
        195                 200                 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
    210                 215                 220
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Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225                 230                 235                 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
                245                 250                 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
            260                 265                 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
        275                 280                 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
    290                 295                 300

Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305                 310                 315                 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
                325                 330                 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
            340                 345                 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
        355                 360                 365

Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
    370                 375                 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385                 390                 395                 400

Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
                405                 410                 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
            420                 425                 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
        435                 440                 445

Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
    450                 455                 460

Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Leu
465                 470                 475                 480

Ser Met Ile Ser Cys Gln Thr
                485
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<210> 25
<211> 56
<212> PRT
<213> Streptococcus mutans

<400> 25

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Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly Asp
1               5                   10                  15

Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe Gly
            20                  25                  30

Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met Phe
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35 40 45

Asp Phe Met Ile Asn His Ile Ser
50 55

<210> 26
<211> 42
<212> PRT
<213> Streptococcus mutans

<400> 26

Arg Pro Thr Gln Glu Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Arg
1 5 10 15

Ala Pro Lys Gln Glu Ile Gln Phe Ala Asp Gly Ser Val Glu His Leu
20 25 30

Trp Asn Thr Phe Gly Glu Glu Gln Ile Asp
35 40

<210> 27
<211> 38
<212> PRT
<213> Streptococcus mutans

<400> 27

Ile Leu Pro Glu Ile His Glu His Tyr Thr Ile Gln Phe Lys Ile Ala
1 5 10 15

Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala Leu Pro Met Val Thr Leu
20 25 30

Tyr Ser Leu Tyr Ser Gly
35